

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Robertson et al.
- (ii) TITLE OF INVENTION: Catalases
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
 - (B) STREET: 6 BECKER FARM ROAD
 - (C) CITY: ROSELAND
 - (D) STATE: NEW JERSEY
 - (E) COUNTRY: USA
 - (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 INCH DISKETTE
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/674,887
 - (B) FILING DATE: July 3, 1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Charles J. Herron
 - (B) REGISTRATION NUMBER: 28,019
 - (C) REFERENCE/DOCKET NUMBER: 331400-55
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAATAAC GCATCCGCTG AC

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEIC ACID
 - (B) TYPE: NUCLEOTIDES
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAAGCTT TTACGACGCG ACGTCGAAAC G

31

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATTAAAGAGG AGAAATTAAAC TATGGAAAAT CACAAACACT CA

52

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGAAGGTACC TTATTTCAGA TCAACCGGT C

31

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 2262 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AAT AAC GCA TCC GCT GAC GAT CTA CAC AGT AGC TTG CAG CAA AGA 48
Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Arg
5 10 15

TGC AGA GCA TTT GTT CCC TTG GTA TCG CCA AGG CAT AGA GCA ATA AGG 96
Cys Arg Ala Phe Val Pro Leu Val Ser Pro Arg His Arg Ala Ile Arg
20 25 30

GAG AGA GCT ATG AGC GGT AAA TGT CCT GTC ATG CAC GGT GGT AAC ACC 144
Glu Arg Ala Met Ser Gly Lys Cys Pro Val Met His Gly Gly Asn Thr
35 40 45

| | |
|---|-----|
| TCG ACC GGT ACT TCC AAC AAA GAT TGG TGG CCG GAA GGG TTG AAC CTG Ser Thr Gly Thr Ser Asn Lys Asp Trp Trp Pro Glu Gly Leu Asn Leu 50 | 192 |
| GAT ATT TTG CAT CAG CAA GAT CGC AAA TCA GAC ATG GAT CCG GAT Asp Ile Leu His Gln Gln Asp Arg Lys Ser Asp Pro Met Asp Pro Asp 65 | 240 |
| TTC AAC TAC CGT GAA GAA GTA CGC AAG CTC GAT TTC GAC GCG CTG AAG Phe Asn Tyr Arg Glu Glu Val Arg Lys Leu Asp Phe Asp Ala Leu Lys 85 | 288 |
| AAA GAT GTC CAC GCG TTG ATG ACC GAT AGC CAA GAG TGG TGG CCC GCT Lys Asp Val His Ala Leu Met Thr Asp Ser Gln Glu Trp Trp Pro Ala 100 | 336 |
| GAC TGG GGG CAC TAC GGC GGT TTG ATG ATC CGT ATG GCT TGG CAC TCC Asp Trp Gly His Tyr Gly Gly Leu Met Ile Arg Met Ala Trp His Ser 115 | 384 |
| GCT GGC ACC TAC CGT ATT GCT GAT GGC CGT GGG GGC GGT GGT ACC GGA Ala Gly Thr Tyr Arg Ile Ala Asp Gly Arg Gly Gly Gly Thr Gly 130 | 432 |
| AGC CAG CGC TTT GCA CCG CTC AAC TCC TGG CCG GAC AAC GTC AGC CTG Ser Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn Val Ser Leu 145 | 480 |
| GAT AAA GCG CGC CGT CTG CTG TGG CCG ATC AAG AAG AAG TAC GGC AAC Asp Lys Ala Arg Arg Leu Leu Trp Pro Ile Lys Lys Lys Tyr Gly Asn 165 | 528 |
| AAA ATC AGC TGG GCA GAC CTG ATG ATT CTG GCT GGC ACC GTG GCT TAT Lys Ile Ser Trp Ala Asp Leu Met Ile Leu Ala Gly Thr Val Ala Tyr 180 | 576 |
| GAG TCC ATG GGC TTA CCT GCT TAC GGC TTC TCT TTC GGC CCG GTC GAT Glu Ser Met Gly Leu Pro Ala Tyr Gly Phe Ser Phe Gly Arg Val Asp 195 | 624 |
| ATT TGG GAA CCC GAA AAA GAT ATC TAC TGG GGT GAC GAA AAA GAG TGG Ile Trp Glu Pro Glu Lys Asp Ile Tyr Trp Gly Asp Glu Lys Glu Trp 210 | 672 |
| CTG GCA CCT TCT GAC GAA CGC TAC GGC GAC GTG AAC AAG CCA GAG ACC Leu Ala Pro Ser Asp Glu Arg Tyr Gly Asp Val Asn Lys Pro Glu Thr 225 | 720 |
| ATG GAA AAC CCG CTG GCG GCT GTC CAA ATG GGT CTG ATC TAT GTG AAC Met Glu Asn Pro Leu Ala Ala Val Gln Met Gly Leu Ile Tyr Val Asn 245 | 768 |
| CCG GAA GGT GTT AAC GGC CAC CCT GAT CCG CTG AGA ACC GCA CAG CAG Pro Glu Gly Val Asn Gly His Pro Asp Pro Leu Arg Thr Ala Gln Gln 260 | 816 |
| GTA CTT GAA ACC TTC GCC CGT ATG GCG ATG AAC GAC GAA AAA ACC GCA Val Leu Glu Thr Phe Ala Arg Met Ala Met Asn Asp Glu Lys Thr Ala 275 | 864 |
| GCC CTC ACA GCT GGC GGC CAC ACC GTC GGT AAT TGT CAC GGT AAT GGC Ala Leu Thr Ala Gly His Thr Val Gly Asn Cys His Gly Asn Gly 290 | 912 |
| AAT GCC TCT GCG TTA GCC CCT GAC CCA AAA GCC TCT GAC GTT GAA AAC Asn Ala Ser Ala Leu Ala Pro Asp Pro Lys Ala Ser Asp Val Glu Asn 305 | 960 |

| | |
|---|------|
| CAG GGC TTA GGT TGG GGC AAC CCC AAC ATG CAG GGC AAG GCA AGC AAC Gln Gly Leu Gly Trp Gly Asn Pro Asn Met Gln Gly Lys Ala Ser Asn 325 330 335 | 1008 |
| GCC GTG ACC TCG GGT ATC GAA GGT GCT TGG ACC ACC AAC CCC ACG AAA Ala Val Thr Ser Gly Ile Glu Gly Ala Trp Thr Thr Trp Glu Lys 340 345 350 | 1056 |
| TTC GAT ATG GGC TAT TTC GAC CTG CTG TTC GGC TAC AAT TGG GAA CTG Phe Asp Met Gly Tyr Phe Asp Leu Leu Phe Gly Tyr Asn Trp Glu Leu 355 360 365 | 1104 |
| AAA AAG AGT CCT GCC GGT GCC CAC CAT TGG GAA CCG ATT GAC ATC AAA Lys Lys Ser Pro Ala Gly Ala His His Trp Glu Pro Ile Asp Ile Lys 370 375 380 | 1152 |
| AAG GAA AAC AAG CCG GTT GAC GCC AGC GAC CCC TCT ATT CGC CAC AAC Lys Glu Asn Lys Pro Val Asp Ala Ser Asp Pro Ser Ile Arg His Asn 385 390 395 400 | 1200 |
| CCG ATC ATG ACC GAT GCG GAT ATG GCG ATA AAG GTA AAT CCG ACC TAT Pro Ile Met Thr Asp Ala Asp Met Ala Ile Lys Val Asn Pro Thr Tyr 405 410 415 | 1248 |
| GCG GCT ATC TGC GAA AAA TTC ATG GCC GAT CCT GAG TAC TTC AAG AAA Arg Ala Ile Cys Glu Lys Phe Met Ala Asp Pro Glu Tyr Phe Lys Lys 420 425 430 | 1296 |
| ACT TTC GCG AAG GCG TGG TTC AAG CTG ACG CAC CGT GAC CTG GGC CCG Thr Phe Ala Lys Ala Trp Phe Lys Leu Thr His Arg Asp Leu Gly Pro 435 440 445 | 1344 |
| AAA TCA CGT TAC ATC GGC CCG GAA GTG CCG GCA GAA GAC CTG ATT TGG Lys Ser Arg Tyr Ile Gly Pro Glu Val Pro Ala Glu Asp Leu Ile Trp 450 455 460 | 1392 |
| GAA GAC CCG ATT CCG GCA GGT AAC ACC GAC TAC TGC GAA GAA GTG GTC Gln Asp Pro Ile Pro Ala Gly Asn Thr Asp Tyr Cys Glu Glu Val Val 465 470 475 480 | 1440 |
| AAG CAG AAA ATT GCA CAA AGT GGC CTG AGC ATT AGT GAG ATG GTC TCC Lys Gln Lys Ile Ala Gln Ser Gly Leu Ser Ile Ser Glu Met Val Ser 485 490 495 | 1488 |
| ACC GCT TGG GAC AGT GCC CGT ACT TAT CGC GGT TCC GAT ATG CGC GGC Thr Ala Trp Asp Ser Ala Arg Thr Tyr Arg Gly Ser Asp Met Arg Gly 500 505 510 | 1536 |
| GGT GCT AAC GGT GCC CGC ATT CGC TTG GCC CCA CAG AAC GAG TGG CAG Gly Ala Asn Gly Ala Arg Ile Arg Leu Ala Pro Gln Asn Glu Trp Gln 515 520 525 | 1584 |
| GGC AAC GAG CCG GAG CGC CTG GCG AAA GTG CTG AGC GTC TAC GAG CAG Gly Asn Glu Pro Glu Arg Leu Ala Lys Val Leu Ser Val Tyr Glu Gln 530 535 540 | 1632 |
| ATC TCT GCC GAC ACC GGC GCT AGC ATC GCG GAC GTG ATC GTT CTG GCC Ile Ser Ala Asp Thr Gly Ala Ser Ile Ala Asp Val Ile Val Leu Ala 545 550 555 560 | 1680 |
| GGT AGC GTA GGC ATC GAG AAA GCC GCG AAA GCA GCA GGT TAC GAT GTG Gly Ser Val Gly Ile Glu Lys Ala Ala Lys Ala Ala Gly Tyr Asp Val 565 570 575 | 1728 |
| GCG GTT CCC TTC CTG AAA GGC CGT GGC GAT GCG ACC GCC GAG ATG ACC Arg Val Pro Phe Leu Lys Gly Arg Gly Asp Ala Thr Ala Glu Met Thr 580 585 590 | 1776 |

| | |
|---|------|
| GAC GCA GAC TTC TTC GCA CCG CTG GAG CCG CTG GCC GAT GGC TTC CGC Asp Ala Asp Ser Phe Ala Pro Leu Glu Pro Leu Ala Asp Gly Phe Arg 595 600 605 | 1824 |
| AAC TGG CAG AAG AAA GAG TAT GTG GTG AAG CCG GAA GAG ATG CTG CTG Asn Trp Gln Lys Lys Glu Tyr Val Val Lys Pro Glu Glu Met Leu Leu 610 615 620 | 1872 |
| GAT GGT GCG CAG CTG ATG GGC TTA ACC GGC CCG GAA ATG ACC GTG CTG Asp Arg Ala Gln Leu Met Gly Leu Thr Gly Pro Glu Met Thr Val Leu 625 630 635 640 | 1920 |
| CTG GGC GGT ATG CGC GTA CTG GGC ACC AAC TAT GGT GGC ACC AAA CAC Leu Gly Gly Met Arg Val Leu Gly Thr Asn Tyr Gly Gly Thr Lys His 645 650 655 | 1968 |
| GGC GTA TTC ACC GAT TGT GAA GGC CAG TTG ACC AAC GAC TTT TTT GTG Gly Val Phe Asp Asp Cys Glu Gly Leu Thr Asn Asp Phe Phe Val 655 660 665 | 2016 |
| AAC CTG ACC GAT ATG GGG AAC AGC TGG AAG CCG GTA GGT AGC AAC GCC Asn Leu Thr Asp Met Gly Asn Ser Trp Lys Pro Val Gly Ser Asn Ala 670 675 680 | 2064 |
| TAC GAA ATC CGC GAC CGC AAG ACC GGT GCC GTG AAG TGG ACC GCC TCG Tyr Glu Ile Arg Asp Arg Lys Thr Gly Ala Val Lys Trp Thr Ala Ser 685 690 700 | 2112 |
| CGC GTG GAT CTG GTA TTT GGT TCC AAC TCG CTA CTG CGC TCT TAC GCA Arg Val Asp Leu Val Phe Gly Ser Asn Ser Leu Leu Arg Ser Tyr Ala 705 710 715 720 | 2160 |
| GAA GTG TAC GCC CAG GAC GAT AAC GGC GAG AAG TTC GTC AGA GAC TTC Glu Val Tyr Ala Gln Asp Asp Asn Gly Glu Lys Phe Val Arg Asp Phe 725 730 735 | 2208 |
| GTC GCC GCC TGG ACC AAA GTG ATG AAC GCC GAC CGT TTC GAC GTC GCG Val Ala Ala Trp Thr Lys Val Met Asn Ala Asp Arg Phe Asp Val Ala 740 745 750 | 2256 |
| TCG TAA Ser | 2262 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 753 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| |
|---|
| Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Arg 5 10 15 |
| Cys Arg Ala Phe Val Pro Leu Val Ser Pro Arg His Arg Ala Ile Arg 20 25 30 |
| Glu Arg Ala Met Ser Gly Lys Cys Pro Val Met His Gly Asn Thr 35 40 45 |

Ser Thr Gly Thr Ser Asn Lys Asp Trp Trp Pro Glu Gly Leu Asn Leu
 50 55 60
 Asp Ile Leu His Gln Gln Asp Arg Lys Ser Asp Pro Met Asp Pro Asp
 65 70 75 80
 Phe Asn Tyr Arg Glu Glu Val Arg Lys Leu Asp Phe Asp Ala Leu Lys
 85 90 95
 Lys Asp Val His Ala Leu Met Thr Asp Ser Gln Glu Trp Trp Pro Ala
 100 105 110
 Asp Trp Gly His Tyr Gly Gly Leu Met Ile Arg Met Ala Trp His Ser
 115 120 125
 Ala Gly Thr Tyr Arg Ile Ala Asp Gly Arg Gly Gly Gly Thr Gly
 130 135 140
 Ser Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn Val Ser Leu
 145 150 155 160
 Asp Lys Ala Arg Arg Leu Leu Trp Pro Ile Lys Lys Lys Tyr Gly Asn
 165 170 175
 Lys Ile Ser Trp Ala Asp Leu Met Ile Leu Ala Gly Thr Val Ala Tyr
 180 185 190
 Glu Ser Met Gly Leu Pro Ala Tyr Gly Phe Ser Phe Gly Arg Val Asp
 195 200 205
 Ile Trp Glu Pro Glu Lys Asp Ile Tyr Trp Gly Asp Glu Lys Glu Trp
 210 215 220
 Leu Ala Pro Ser Asp Glu Arg Tyr Gly Asp Val Asn Lys Pro Glu Thr
 225 230 235 240
 Met Glu Asn Pro Leu Ala Ala Val Gln Met Gly Leu Ile Tyr Val Asn
 245 250 255
 Pro Glu Gly Val Asn Gly His Pro Asp Pro Leu Arg Thr Ala Gln Gln
 260 265 270
 Val Leu Glu Thr Phe Ala Arg Met Ala Met Asn Asp Glu Lys Thr Ala
 275 280 285
 Ala Leu Thr Ala Gly Gly His Thr Val Gly Asn Cys His Gly Asn Gly
 290 295 300
 Asn Ala Ser Ala Leu Ala Pro Asp Pro Lys Ala Ser Asp Val Glu Asn
 305 310 315 320
 Gln Gly Leu Gly Trp Gly Asn Pro Asn Met Gln Gly Lys Ala Ser Asn
 325 330 335
 Ala Val Thr Ser Gly Ile Glu Gly Ala Trp Thr Thr Asn Pro Thr Lys
 340 345 350
 Phe Asp Met Gly Tyr Phe Asp Leu Leu Phe Gly Tyr Asn Trp Glu Leu
 355 360 365
 Lys Lys Ser Pro Ala Gly Ala His His Trp Glu Pro Ile Asp Ile Lys
 370 375 380
 Lys Glu Asn Lys Pro Val Asp Ala Ser Asp Pro Ser Ile Arg His Asn
 385 390 395 400

Pro Ile Met Thr Asp Ala Asp Met Ala Ile Lys Val Asn Pro Thr Tyr
 405 410 415
 Arg Ala Ile Cys Glu Lys Phe Met Ala Asp Pro Glu Tyr Phe Lys Lys
 420 425 430
 Thr Phe Ala Lys Ala Trp Phe Lys Leu Thr His Arg Asp Leu Gly Pro
 435 440 445
 Lys Ser Arg Tyr Ile Gly Pro Glu Val Pro Ala Glu Asp Leu Ile Trp
 450 455 460
 Gln Asp Pro Ile Pro Ala Gly Asn Thr Asp Tyr Cys Glu Glu Val Val
 465 470 475 480
 Lys Gln Lys Ile Ala Gln Ser Gly Leu Ser Ile Ser Glu Met Val Ser
 485 490 495
 Thr Ala Trp Asp Ser Ala Arg Thr Tyr Arg Gly Ser Asp Met Arg Gly
 500 505 510
 Gly Ala Asn Gly Ala Arg Ile Arg Leu Ala Pro Gln Asn Glu Trp Gln
 515 520 525
 Gly Asn Glu Pro Glu Arg Leu Ala Lys Val Leu Ser Val Tyr Glu Gln
 530 535 540
 Ile Ser Ala Asp Thr Gly Ala Ser Ile Ala Asp Val Ile Val Leu Ala
 545 550 555 560
 Gly Ser Val Gly Ile Glu Lys Ala Ala Lys Ala Ala Gly Tyr Asp Val
 565 570 575
 Arg Val Pro Phe Leu Lys Gly Arg Gly Asp Ala Thr Ala Glu Met Thr
 580 585 590
 Asp Ala Asp Ser Phe Ala Pro Leu Glu Pro Leu Ala Asp Gly Phe Arg
 595 600 605
 Asn Trp Gln Lys Lys Glu Tyr Val Val Lys Pro Glu Glu Met Leu Leu
 610 615 620
 Asp Arg Ala Gln Leu Met Gly Leu Thr Gly Pro Glu Met Thr Val Leu
 625 630 635 640
 Leu Gly Gly Met Arg Val Leu Gly Thr Asn Tyr Gly Gly Thr Lys His
 645 650 655
 Gly Val Phe Thr Asp Cys Glu Gly Gln Leu Thr Asn Asp Phe Phe Val
 660 665 670
 Asn Leu Thr Asp Met Gly Asn Ser Trp Lys Pro Val Gly Ser Asn Ala
 675 680 685
 Tyr Glu Ile Arg Asp Arg Lys Thr Gly Ala Val Lys Trp Thr Ala Ser
 690 695 700
 Arg Val Asp Leu Val Phe Gly Ser Asn Ser Leu Leu Arg Ser Tyr Ala
 705 710 715 720
 Glu Val Tyr Ala Gln Asp Asp Asn Gly Glu Lys Phe Val Arg Asp Phe
 725 730 735
 Val Ala Ala Trp Thr Lys Val Met Asn Ala Asp Arg Phe Asp Val Ala
 740 745 750
 Ser

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 2238 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GAA | AAT | CAC | AAA | CAC | TCA | GGA | TCT | TCT | ACG | TAT | AAC | ACA | AAC | ACT | 48 |
| Met | Glu | Asn | His | Lys | His | Ser | Gly | Ser | Ser | Thr | Tyr | Asn | Thr | Asn | Thr | |
| | | | | 5 | | | | | 10 | | | | | 15 | | |
| GGC | GGA | AAA | TGC | CCT | TTT | ACC | GGA | GGT | TCG | CTT | AAG | CAA | AGT | GCA | GGT | 96 |
| Gly | Gly | Lys | Cys | Pro | Phe | Thr | Gly | Gly | Ser | Leu | Lys | Gln | Ser | Ala | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GGC | GGC | ACC | AAA | AAC | AGG | GAT | TGG | TGG | CCC | AAC | ATG | CTC | AAC | CTC | GGC | 144 |
| Gly | Gly | Thr | Lys | Asn | Arg | Asp | Trp | Trp | Pro | Asn | Met | Leu | Asn | Leu | Gly | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| ATC | TTA | CGC | CAA | CAT | TCA | TCG | CTA | TCG | GAC | CCA | AAC | GAC | CCG | GAT | TTT | 192 |
| Ile | Leu | Arg | Gln | His | Ser | Ser | Leu | Ser | Asp | Pro | Asn | Asp | Pro | Asp | Phe | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |
| GAC | TAT | GCC | GAA | GAG | TTT | AAG | AAG | CTA | GAT | CTG | GCA | GCG | GTT | AAA | AAG | 240 |
| Asp | Tyr | Ala | Glu | Glu | Phe | Lys | Lys | Leu | Asp | Leu | Ala | Ala | Val | Lys | Lys | |
| | 65 | | | 70 | | | | 75 | | | | | | 80 | | |
| GAC | CTG | GCA | GCG | CTA | ATG | ACA | GAT | TCA | CAG | GAC | TGG | TGG | CCA | GCA | GAT | 288 |
| Asp | Leu | Ala | Ala | Leu | Met | Thr | Asp | Ser | Gln | Asp | Trp | Trp | Pro | Ala | Asp | |
| | | | | 85 | | | | 90 | | | | | 95 | | | |
| TAC | GGT | CAT | TAT | GGC | CCC | TTC | TTT | ATA | CGC | ATG | GCG | TGG | CAC | AGC | GCC | 336 |
| Tyr | Gly | His | Tyr | Gly | Pro | Phe | Phe | Ile | Arg | Met | Ala | Trp | His | Ser | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| GGC | ACC | TAC | CGT | ATC | GGT | GAT | GGC | CGT | GGT | GGC | GGT | GGC | TCC | GGC | TCA | 384 |
| Gly | Thr | Tyr | Arg | Ile | Gly | Asp | Gly | Arg | Gly | Gly | Gly | Ser | Gly | Ser | | |
| | | | 115 | | | 120 | | | | | | 125 | | | | |
| CAG | CGC | TTC | GCG | CCT | CTC | AAT | AGC | TGG | CCA | GAC | AAT | GCC | AAT | CTG | GAT | 432 |
| Gln | Arg | Phe | Ala | Pro | Leu | Asn | Ser | Trp | Pro | Asp | Asn | Ala | Asn | Leu | Asp | |
| | | | 130 | | | 135 | | | | | 140 | | | | | |
| AAA | GCA | GCG | TTG | CTT | CTT | TGG | CCC | ATC | AAA | CAA | AAA | TAC | GGT | CGA | AAA | 480 |
| Lys | Ala | Arg | Leu | Leu | Leu | Trp | Pro | Ile | Lys | Gln | Lys | Tyr | Gly | Arg | Lys | |
| | | | 145 | | 150 | | | | 155 | | | | | 160 | | |
| ATC | TCC | TGG | GCG | GAT | CTA | ATG | ATA | CTC | ACA | GGA | AAC | GTA | GCT | CTG | GAA | 528 |
| Ile | Ser | Trp | Ala | Asp | Leu | Met | Ile | Leu | Thr | Gly | Asn | Val | Ala | Leu | Glu | |
| | | | 165 | | | | | 170 | | | | | | 175 | | |
| ACT | ATG | GGC | TTT | AAA | ACT | TTT | GGT | TTT | GCA | GGT | GGC | AGA | GCA | GAT | GTA | 576 |
| Thr | Met | Gly | Phe | Lys | Thr | Phe | Gly | Phe | Ala | Gly | Gly | Arg | Ala | Asp | Val | |
| | | | 180 | | | | 185 | | | | | | 190 | | | |
| TGG | GAG | CCT | GAA | GAA | GAT | GTA | TAC | TGG | GGA | GCA | GAA | ACC | GAA | TGG | CTG | 624 |
| Trp | Glu | Pro | Glu | Glu | Asp | Val | Tyr | Trp | Gly | Ala | Glu | Thr | Glu | Trp | Leu | |
| | | | 195 | | | 200 | | | | | | 205 | | | | |

| | |
|---|------|
| GGA GAC AAG CGC TAT GAA GGT GAC CGA GAG CTC GAA AAT CCC CTG GGA Gly Asp Lys Arg Tyr Glu Gly Asp Arg Glu Leu Glu Asn Pro Leu Gly 210 215 220 | 672 |
| GCC GTA CAA ATG GGA CTC ATC TAT GTA AAC CCC GAA GGA CCC AAC GGC Ala Val Gln Met Gly Leu Ile Tyr Val Asn Pro Glu Gly Pro Asn Gly 225 230 235 240 | 720 |
| AAG CCA GAC CCT ATC GCT GCT GCG CGT GAT ATT CGT GAG ACT TTT GGC Lys Pro Asp Pro Ile Ala Ala Arg Asp Ile Arg Glu Thr Phe Gly 245 250 | 768 |
| CGA ATG GCA ATG AAT GAC GAA GAA ACC GTG GCT CTC ATA GCG GGT GGA Arg Met Ala Met Asn Asp Glu Glu Thr Val Ala Leu Ile Ala Gly Gly 260 265 | 816 |
| CAC ACC TTC GGA AAA ACC CAT GGT GCT GCC GAT GCG GAG AAA TAT GTG His Thr Phe Gly Lys Thr His Gly Ala Ala Asp Ala Glu Lys Tyr Val 275 280 | 864 |
| GGC CGA GAG CCT GCC GCC GCA GGT ATT GAA GAA ATG AGC CTG GGG TGG Gly Arg Glu Pro Ala Ala Glu Gly Ile Glu Glu Met Ser Leu Gly Trp 290 295 300 | 912 |
| AAA AAC ACC TAC GGC ACC GGA CAC GGT GCG GAT ACC ATC ACC AGT GGA Lys Asn Thr Tyr Gly Thr Gly His Gly Ala Asp Thr Ile Thr Ser Gly 305 310 315 320 | 960 |
| CTA GAA GGC GCC TGG ACC AAG ACC CCT ACT CAA TGG AGC AAT AAC TTT Leu Glu Gly Ala Trp Thr Lys Thr Pro Thr Gln Trp Ser Asn Asn Phe 325 330 | 1008 |
| TTT GAA AAC CTC TTT GGT TAC GAG TGG GAG CTT ACC AAA AGT CCA GCT Phe Glu Asn Leu Phe Gly Tyr Glu Trp Glu Leu Thr Lys Ser Pro Ala 340 345 350 | 1056 |
| GGA GCT TAT CAG TGG AAA CCA AAA GAC GGT GCC GGG GCT GGC ACC ATA Gly Ala Tyr Gln Trp Lys Pro Lys Asp Gly Ala Gly Ala Gly Thr Ile 355 360 365 | 1104 |
| CCG GAT GCA CAT GAT CCC AGC AAG TCG CAC GCT CCA TTT ATG CTC ACT Pro Asp Ala His Asp Pro Ser Lys Ser His Ala Pro Phe Met Leu Thr 370 375 380 | 1152 |
| ACG GAC CTG GCG CTG CGC ATG GAC CCT GAT TAC GAA AAA ATT TCT CGA Thr Asp Leu Ala Leu Arg Met Asp Pro Asp Tyr Glu Lys Ile Ser Arg 385 390 395 400 | 1200 |
| CGG TAC TAT GAA AAC CCT GAT GAG TTT GCA GAT GCT TTC GCG AAA GCA Arg Tyr Tyr Glu Asn Pro Asp Glu Phe Ala Asp Ala Phe Ala Lys Ala 405 410 415 | 1248 |
| TGG TAC AAA CTG ACA CAC AGA GAT ATG GGA CCA AAG GTG CGC TAC CTG Trp Tyr Lys Leu Thr His Arg Asp Met Gly Pro Lys Val Arg Tyr Leu 420 425 430 | 1296 |
| GGA CCA GAA GTG CCT CAG GAA GAC CTC ATC TGG CAA GAC CCT ATA CCA Gly Pro Glu Val Pro Gln Glu Asp Leu Ile Trp Gln Asp Pro Ile Pro 435 440 445 | 1344 |
| GAT GTA AGC CAT CCT CTT GTA GAC GAA AAC GAT ATT GAA GGC CTA AAA Asp Val Ser His Pro Leu Val Asp Glu Asn Asp Ile Glu Gly Leu Lys 450 455 460 | 1392 |
| GCC AAA ATC CTG GAA TCG GGA CTG ACG GTA AGC GAG CTG GTA AGC ACG Ala Lys Ile Leu Glu Ser Gly Leu Thr Val Ser Glu Leu Val Ser Thr 465 470 475 480 | 1440 |

| | |
|--|------|
| GCA TGG GCT TCT GCA TCT ACT TTT AGA AAC TCT GAC AAG CGC GGC GGT Ala Trp Ala Ser Ala Ser Thr Phe Arg Asn Ser Asp Lys Arg Gly Gly | 1488 |
| 485 500 | |
| GCC AAC GGT GCA CGT ATA CGA CTG GCC CCA CAA AAA GAC TGG GAA GTA Ala Asn Gly Ala Arg Ile Arg Leu Ala Pro Gln Lys Asp Trp Glu Val | 1536 |
| 505 510 | |
| AAC AAC CCT CAG CAA CTT GCC AGG GTA CTC AAA ACA CTA GAA GGT ATC Asn Asn Pro Gln Gln Leu Ala Arg Val Leu Lys Thr Leu Glu Gly Ile | 1584 |
| 520 530 | |
| CAG GAG GAC TTT AAC CAG GCG CAA TCA GAT AAC AAA GCA GTA TCG TTG Gln Glu Asp Phe Asn Gln Ala Gln Ser Asp Asn Lys Ala Val Ser Leu | 1632 |
| 535 540 | |
| GCC GAC CTG ATT GTG CTG GCC GGC TGT GCG GGT GTA GAA AAA GCT GCA Ala Asp Leu Ile Val Leu Ala Gly Cys Ala Gly Val Glu Lys Ala Ala | 1680 |
| 550 555 | |
| AAA GAT GCT GGC CAT GAG GTG CAG GTG CCT TTC AAC CCG GGA CGA GCG Lys Asp Ala Gly His Glu Val Gln Val Pro Phe Asn Pro Gly Arg Ala | 1728 |
| 570 575 | |
| GAT GCC ACC GCT GAG CAA ACC GAT GTG GAA GCT TTC GAA GCA CTA GAG Asp Ala Thr Glu Gln Thr Asp Val Glu Ala Phe Glu Ala Leu Glu | 1776 |
| 585 590 | |
| CGA GCG GCT GAC GGC TTT AGA AAC TAC ATT AAA CCG GAG CAT AAA GTA Pro Ala Ala Asp Gly Phe Arg Asn Tyr Ile Lys Pro Glu His Lys Val | 1824 |
| 600 605 | |
| TCC GCT GAG GAA ATG CTC GTA GAC CGG GCG CAG CTT CTG TCG CTT TCG Ser Ala Glu Glu Met Leu Val Asp Arg Ala Gln Leu Leu Ser Leu Ser | 1872 |
| 615 620 | |
| GCA CCA GAA ATG ACT GCT TTG GTA GGC GGT ATG CGT GTA CTG GGC ACC Ala Pro Glu Met Thr Ala Leu Val Gly Gly Met Arg Val Leu Gly Thr | 1920 |
| 630 635 | |
| AAC TAC GAC GGT TCG CAG CAT GGA GTG TTT ACA AAT AAG CCG GGT CAG Asn Tyr Asp Gly Ser Gln His Gly Val Phe Thr Asn Lys Pro Gly Gln | 1968 |
| 650 655 | |
| CTA TCC AAT GAC TTC TTT GTA AAC CTG CTA GAC CTC AAC ACT AAA TGG Leu Ser Asn Asp Phe Phe Val Asn Leu Leu Asp Leu Asn Thr Lys Trp | 2016 |
| 665 670 | |
| CGA GCC AGC GAT GAA TCA GAC AAA GIT TTT GAA GGC AGA GAC TTC AAA Arg Ala Ser Asp Glu Ser Asp Lys Val Phe Glu Gly Arg Asp Phe Lys | 2064 |
| 680 685 | |
| ACT GGC GAA GTA AAG TGG AGT GGC ACC CGG GTA GAC CTG ATC TTC GGA Thr Gly Glu Val Lys Trp Ser Gly Thr Arg Val Asp Leu Ile Phe Gly | 2112 |
| 695 700 | |
| TCC AAT TCC GAG CTA AGA GCC CTC GCA GAA GTG TAC GGC TGT GCA GAT Ser Asn Ser Glu Leu Arg Ala Leu Ala Glu Val Tyr Gly Cys Ala Asp | 2160 |
| 715 720 | |
| TCT GAA GAA AAG TTT GTT AAA GAT TTT GTG AAG GCC TGG GCC AAA GTA Ser Glu Glu Lys Phe Val Lys Asp Phe Val Lys Ala Trp Ala Lys Val | 2208 |
| 735 740 | |
| ATG GAC CTG GAC CGG TTT GAT CTG AAA TAA Met Asp Leu Asp Arg Phe Asp Leu Lys | 2238 |
| 750 755 | |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 745 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Asn His Lys His Ser Gly Ser Ser Thr Tyr Asn Thr Asn Thr
5 10 15
Gly Gly Lys Cys Pro Phe Thr Gly Gly Ser Leu Lys Gln Ser Ala Gly
20 25 30
Gly Gly Thr Lys Asn Arg Asp Trp Trp Pro Asn Met Leu Asn Leu Gly
35 40 45
Ile Leu Arg Gln His Ser Ser Leu Ser Asp Pro Asn Asp Pro Asp Phe
50 55 60
Asp Tyr Ala Glu Glu Phe Lys Lys Leu Asp Leu Ala Ala Val Lys Lys
65 70 75
Asp Leu Ala Ala Leu Met Thr Asp Ser Gln Asp Trp Trp Pro Ala Asp
85 90 95
Tyr Gly His Tyr Gly Pro Phe Phe Ile Arg Met Ala Trp His Ser Ala
100 105 110
Gly Thr Tyr Arg Ile Gly Asp Gly Arg Gly Gly Gly Ser Gly Ser
115 120 125
Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn Ala Asn Leu Asp
130 135 140
Lys Ala Arg Leu Leu Leu Trp Pro Ile Lys Gln Lys Tyr Gly Arg Lys
145 150 155 160
Ile Ser Trp Ala Asp Leu Met Ile Leu Thr Gly Asn Val Ala Leu Glu
165 170 175
Thr Met Gly Phe Lys Thr Phe Gly Phe Ala Gly Gly Arg Ala Asp Val
180 185 190
Trp Glu Pro Glu Glu Asp Val Tyr Trp Gly Ala Glu Thr Glu Trp Leu
195 200 205
Gly Asp Lys Arg Tyr Glu Gly Asp Arg Glu Leu Glu Asn Pro Leu Gly
210 215 220
Ala Val Gln Met Gly Leu Ile Tyr Val Asn Pro Glu Gly Pro Asn Gly
225 230 235 240
Lys Pro Asp Pro Ile Ala Ala Ala Arg Asp Ile Arg Glu Thr Phe Gly
245 250 255
Arg Met Ala Met Asn Asp Glu Glu Thr Val Ala Leu Ile Ala Gly Gly
260 265 270
His Thr Phe Gly Lys Thr His Gly Ala Ala Asp Ala Glu Lys Tyr Val
275 280 285

Gly Arg Glu Pro Ala Ala Ala Gly Ile Glu Glu Met Ser Leu Gly Trp
 290 295 300
 Lys Asn Thr Tyr Gly Thr Gly His Gly Ala Asp Thr Ile Thr Ser Gly
 305 310 315 320
 Leu Glu Gly Ala Trp Thr Lys Thr Pro Thr Gln Trp Ser Asn Asn Phe
 325 330 335
 Phe Glu Asn Leu Phe Gly Tyr Glu Trp Glu Leu Thr Lys Ser Pro Ala
 340 345 350
 Gly Ala Tyr Gln Trp Lys Pro Lys Asp Gly Ala Gly Ala Gly Thr Ile
 355 360 365
 Pro Asp Ala His Asp Pro Ser Lys Ser His Ala Pro Phe Met Leu Thr
 370 375 380
 Thr Asp Leu Ala Leu Arg Met Asp Pro Asp Tyr Glu Lys Ile Ser Arg
 385 390 395 400
 Arg Tyr Tyr Glu Asn Pro Asp Glu Phe Ala Asp Ala Phe Ala Lys Ala
 405 410 415
 Trp Tyr Lys Leu Thr His Arg Asp Met Gly Pro Lys Val Arg Tyr Leu
 420 425 430
 Gly Pro Glu Val Pro Gln Glu Asp Leu Ile Trp Gln Asp Pro Ile Pro
 435 440 445
 Asp Val Ser His Pro Leu Val Asp Glu Asn Asp Ile Glu Gly Leu Lys
 450 455 460
 Ala Lys Ile Leu Glu Ser Gly Leu Thr Val Ser Glu Leu Val Ser Thr
 465 470 475 480
 Ala Trp Ala Ser Ala Ser Thr Phe Arg Asn Ser Asp Lys Arg Gly Gly
 485 490 495
 Ala Asn Gly Ala Arg Ile Arg Leu Ala Pro Gln Lys Asp Trp Glu Val
 500 505 510
 Asn Asn Pro Gln Gln Leu Ala Arg Val Leu Lys Thr Leu Glu Gly Ile
 515 520 525
 Gln Glu Asp Phe Asn Gln Ala Gln Ser Asp Asn Lys Ala Val Ser Leu
 530 535 540
 Ala Asp Leu Ile Val Leu Ala Gly Cys Ala Gly Val Glu Lys Ala Ala
 545 550 555 560
 Lys Asp Ala Gly His Glu Val Gln Val Pro Phe Asn Pro Gly Arg Ala
 565 570 575
 Asp Ala Thr Ala Glu Gln Thr Asp Val Glu Ala Phe Glu Ala Leu Glu
 580 585 590
 Pro Ala Ala Asp Gly Phe Arg Asn Tyr Ile Lys Pro Glu His Lys Val
 595 600 605
 Ser Ala Glu Glu Met Leu Val Asp Arg Ala Gln Leu Leu Ser Leu Ser
 610 615 620
 Ala Pro Glu Met Thr Ala Leu Val Gly Gly Met Arg Val Leu Gly Thr
 625 630 635 640

Asn Tyr Asp Gly Ser Gln His Gly Val Phe Thr Asn Lys Pro Gly Gln
 645 650 655
 Leu Ser Asn Asp Phe Phe Val Asn Leu Leu Asp Leu Asn Thr Lys Trp
 660 665 670
 Arg Ala Ser Asp Glu Ser Asp Lys Val Phe Glu Gly Arg Asp Phe Lys
 675 680
 Thr Gly Glu Val Lys Trp Ser Gly Thr Arg Val Asp Leu Ile Phe Gly
 690 695 700
 Ser Asn Ser Glu Leu Arg Ala Leu Ala Glu Val Tyr Gly Cys Ala Asp
 705 710 715 720
 Ser Glu Glu Lys Phe Val Lys Asp Phe Val Lys Ala Trp Ala Lys Val
 725 730 735
 Met Asp Leu Asp Arg Phe Asp Leu Lys
 740 745

W:\A\281010.SEG

0
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000
 1001
 1002
 1003
 1004
 1005
 1006
 1007
 1008
 1009
 1010
 1011
 1012
 1013
 1014
 1015
 1016
 1017
 1018
 1019
 1020
 1021
 1022
 1023
 1024
 1025
 1026
 1027
 1028
 1029
 1030
 1031
 1032
 1033
 1034
 1035
 1036
 1037
 1038
 1039
 1040
 1041
 1042
 1043
 1044
 1045
 1046
 1047
 1048
 1049
 1050
 1051
 1052
 1053
 1054
 1055
 1056
 1057
 1058
 1059
 1060
 1061
 1062
 1063
 1064
 1065
 1066
 1067
 1068
 1069
 1070
 1071
 1072
 1073
 1074
 1075
 1076
 1077
 1078
 1079
 1080
 1081
 1082
 1083
 1084
 1085
 1086
 1087
 1088
 1089
 1090
 1091
 1092
 1093
 1094
 1095
 1096
 1097
 1098
 1099
 1100
 1101
 1102
 1103
 1104
 1105
 1106
 1107
 1108
 1109
 1110
 1111
 1112
 1113
 1114
 1115
 1116
 1117
 1118
 1119
 1120
 1121
 1122
 1123
 1124
 1125
 1126
 1127
 1128
 1129
 1130
 1131
 1132
 1133
 1134
 1135
 1136
 1137
 1138
 1139
 1140
 1141
 1142
 1143
 1144
 1145
 1146
 1147
 1148
 1149
 1150
 1151
 1152
 1153
 1154
 1155
 1156
 1157
 1158
 1159
 1160
 1161
 1162
 1163
 1164
 1165
 1166
 1167
 1168
 1169
 1170
 1171
 1172
 1173
 1174
 1175
 1176
 1177
 1178
 1179
 1180
 1181
 1182
 1183
 1184
 1185
 1186
 1187
 1188
 1189
 1190
 1191
 1192
 1193
 1194
 1195
 1196
 1197
 1198
 1199
 1200
 1201
 1202
 1203
 1204
 1205
 1206
 1207
 1208
 1209
 1210
 1211
 1212
 1213
 1214
 1215
 1216
 1217
 1218
 1219
 1220
 1221
 1222
 1223
 1224
 1225
 1226
 1227
 1228
 1229
 1230
 1231
 1232
 1233
 1234
 1235
 1236
 1237
 1238
 1239
 1240
 1241
 1242
 1243
 1244
 1245
 1246
 1247
 1248
 1249
 1250
 1251
 1252
 1253
 1254
 1255
 1256
 1257
 1258
 1259
 1260
 1261
 1262
 1263
 1264
 1265
 1266
 1267
 1268
 1269
 1270
 1271
 1272
 1273
 1274
 1275
 1276
 1277
 1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302
 1303
 1304
 1305
 1306
 1307
 1308
 1309
 1310
 1311
 1312
 1313
 1314
 1315
 1316
 1317
 1318
 1319
 1320
 1321
 1322
 1323
 1324
 1325
 1326
 1327
 1328
 1329
 1330
 1331
 1332
 1333
 1334
 1335
 1336
 1337
 1338
 1339
 1340
 1341
 1342
 1343
 1344
 1345
 1346
 1347
 1348
 1349
 1350
 1351
 1352
 1353
 1354
 1355
 1356
 1357
 1358
 1359
 1360
 1361
 1362
 1363
 1364
 1365
 1366
 1367
 1368
 1369
 1370
 1371
 1372
 1373
 1374
 1375
 1376
 1377
 1378
 1379
 1380
 1381
 1382
 1383
 1384
 1385
 1386
 1387
 1388
 1389
 1390
 1391
 1392
 1393
 1394
 1395
 1396
 1397
 1398
 1399
 1400
 1401
 1402
 1403
 1404
 1405
 1406
 1407
 1408
 1409
 1410
 1411
 1412
 1413
 1414
 1415
 1416
 1417
 1418
 1419
 1420
 1421
 1422
 1423
 1424
 1425
 1426
 1427
 1428
 1429
 1430
 1431
 1432
 1433
 1434
 1435
 1436
 1437
 1438
 1439
 1440
 1441
 1442
 1443
 1444
 1445
 1446
 1447
 1448
 1449
 1450
 1451
 1452
 1453
 1454